

GenCore version 5.1.6
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DM nucleic - nucleic search, using sw model

Run on: December 3, 2003, 09:21:18 ; Search time 4 Seconds
(without alignments)
4.181 Million cell updates/sec

Title: A81835

Perfect score: 2787

Sequence: 1 ATGAAGTCTTCTTCCCAA.....GAGCAAAATACCAATCTAA 2787

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 3000 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Database : us-09-428-122-1.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2775.8	99.6	3000	1	us-09-428-122-1

ALIGNMENTS

RESULT 1					
us-09-428-122-1					
Query Match 99.6%; Score 2775.8; DB 1; Length 3000;					
Best Local Similarity 99.7%; Pred. No. 0;					
Matches 2780; Conservative 0; Mismatches 7; Indels 0; Gaps 0;					
QY	1	ATGAAGTCTTCTTCCCAAAGTTTGTATTTCTACATTTGCTATTTTCCCTTTCTGCTATG	60		
DB	101	ATGAAGTCTTCTTCCCAAAGTTTGTATTTCTACATTTGCTATTTTCCCTTTCTGCTATG	160		
QY	61	ATTGCTACCGACAGATTTTGATTCAGTGCAGTTTCGATGGGAATAAAATGGTAAT	120		
DB	161	ATTGCTACCGACAGATTTTGATTCAGTGCAGTTTCGATGGGAATAAAATGGTAAT	220		
QY	121	TTTTCAGTTTCGTCAGAGTCAGAGATGCTGGAATCTTACTCTCTATTTTAAAGGGAATGTC	180		
DB	221	TTTTCAGTTTCGTCAGAGTCAGAGATGCTGGAATCTTACTCTCTATTTTAAAGGGAATGTC	280		
QY	181	ACTCTAGAAATATTCCTGGAACAGACACAGCAATCAAAAAGCTGTTTAAACAACACT	240		
DB	281	ACTCTAGAAATATTCCTGGAACAGACACAGCAATCAAAAAGCTGTTTAAACAACACT	340		
QY	241	AAGGGGATTTGACTTTTCAGGTACCGGAACTCTTATTTGTTCCAAACGGTGGATGCA	300		
DB	341	AAGGGGATTTGACTTTTCAGGTACCGGAACTCTTATTTGTTCCAAACGGTGGATGCA	400		

QY	301	GGGACTGTAGCAGGGGCTGCTGTATTAACAGCAGCGCTGTAGATAAAATCTACACGTTTATA	360		
DB	401	GGGACTGTAGCAGGGGCTGCTGTATTAACAGCAGCGCTGTAGATAAAATCTACACGTTTATA	460		
QY	361	GGGTTTCTTCGCTATCTTTTATTTGCTCTCCCTGGAAGTTTCGATAACTACCGGCAAGA	420		
DB	461	GGGTTTCTTCGCTATCTTTTATTTGCTCTCCCTGGAAGTTTCGATAACTACCGGCAAGA	520		
QY	421	GCCGTTAGCTCTCTACGGGTAGCTTCAAGTTTGCACAAAATCTCAGTTTGTCTTTCAGC	480		
DB	521	GCCGTTAGCTCTCTACGGGTAGCTTCAAGTTTGCACAAAATCTCAGTTTGTCTTTCAGC	580		
QY	481	AAAACTTTTCAACGGATAATGCGGTGCTATCACCGCAAAAATCTTTTCATTAACAGGG	540		
DB	581	AAAACTTTTCAACGGATAATGCGGTGCTATCACCGCAAAAATCTTTTCATTAACAGGG	640		
QY	541	ACTCAATGTCAGCTCTGTTTCTGAAAATACCTCTCAAGAAAGCGGAGCATTCAG	600		
DB	641	ACTCAATGTCAGCTCTGTTTCTGAAAATACCTCTCAAGAAAGCGGAGCATTCAG	700		
QY	601	ACTTCOGATGCCCTTACCATTTAGTGAACCAAGGGGAAGTCTCTTTTCTGCAATACT	660		
DB	701	ACTTCOGATGCCCTTACCATTTAGTGAACCAAGGGGAAGTCTCTTTTCTGCAATACT	760		
QY	661	TCTTCGGATTTCTGAGCTGCAATTTTACAGAGCCCTCGGTGACTATTTCTATATATGCT	720		
DB	761	TCTTCGGATTTCTGAGCTGCAATTTTACAGAGCCCTCGGTGACTATTTCTATATATGCT	820		
QY	721	AAAGTTTCTTTTATTGACAAATAGGTCAAGAGCGAGCTCTCTCAACAGGGGGATATG	780		
DB	821	AAAGTTTCTTTTATTGACAAATAGGTCAAGAGCGAGCTCTCTCAACAGGGGGATATG	880		
QY	781	TCAGAGGTGCTATCTGCTTATTAACCTAGTACAGATTAAGCTCACTCCCTCACTGGA	840		
DB	881	TCAGAGGTGCTATCTGCTTATTAACCTAGTACAGATTAAGCTCACTCCCTCACTGGA	940		
QY	841	AATCAGATGTTTACTCTTCAGCAACATATCATCTGACCAACAGCGGGAGGAGCTATATG	900		
DB	941	AATCAGATGTTTACTCTTCAGCAACATATCATCTGACCAACAGCGGGAGGAGCTATATG	1000		
QY	901	AAAAAGCTCGAACTGGCTTCGGAGGACTTACCTATTCAGTGAAGATAGTGCATATGA	960		
DB	1001	AAAAAGCTCGAACTGGCTTCGGAGGACTTACCTATTCAGTGAAGATAGTGCATATGA	1060		
QY	961	GGTACAGCTCTTAAAGGTGAGCCATAGCTATCGAAGATAGTGGGAATGAGTTTATCC	1020		
DB	1061	GGTACAGCTCTTAAAGGTGAGCCATAGCTATCGAAGATAGTGGGAATGAGTTTATCC	1120		
QY	1021	GCCGATAGTGTGACATTTCTTTTATAGGAATACAGTCACTTCTACTCTCTGGGAGC	1080		
DB	1121	GCCGATAGTGTGACATTTCTTTTATAGGAATACAGTCACTTCTACTCTCTGGGAGC	1180		
QY	1081	AATAGAAGTATGATCGACTTAGGAAACGAGTGCAGGATGACAGCTTTCGCTCTGCT	1140		
DB	1181	AATAGAAGTATGATCGACTTAGGAAACGAGTGCAGGATGACAGCTTTCGCTCTGCT	1240		
QY	1141	GCTAGAGCCATCTACTTATGATCCCATTAACATACAGGATCTTCCCAACAGTTACAGAT	1200		
DB	1241	GCTAGAGCCATCTACTTATGATCCCATTAACATACAGGATCTTCCCAACAGTTACAGAT	1300		
QY	1201	GTCTTTAAAGTTAATGAGCTTCGGCAGATTTCTGCACTACAATATACAGGAAATCATC	1260		
DB	1301	GTCTTTAAAGTTAATGAGCTTCGGCAGATTTCTGCACTACAATATACAGGAAATCATC	1360		
QY	1261	TTTCAGAGGAAAAGTTATACAGAGACAGAGCCGCGAGATTCTTAAATCTTACTTCGAAG	1320		
DB	1361	TTTCAGAGGAAAAGTTATACAGAGACAGAGCCGCGAGATTCTTAAATCTTACTTCGAAG	1420		
QY	1321	CTACTACAGCCTGTAACTCTTTTCAGGAGTACTCTTCTTTTAAACATGAGTGACTCTG	1380		
DB	1421	CTACTACAGCCTGTAACTCTTTTCAGGAGTACTCTTCTTTTAAACATGAGTGACTCTG	1480		
QY	1381	CAGACTCAGGCATTTCACTCAACAGGACAGATTTCTGCTCGAAATGGACGTAGGAATCT	1440		

Db	1481	CAGACTCAGGCATTTCACTCAACAGGCGAATTTCTGGTCTCGAAATGACGCTAGGAACCTACT	1540
Qy	1441	CTAGAACCTCTGATACTAGCAACATTAACAAATTTGGTCAATTAACATCAGTTCTTATAGAC	1500
Db	1541	CTAGAACCTCTGATACTAGCAACATTAACAAATTTGGTCAATTAACATCAGTTCTTATAGAC	1600
Qy	1501	GGTCCAAAGGAAGCAAAATATAGAAACCAAGCTAGCTCAAAAAATCTGACTTTATCTGGA	1560
Db	1601	GGTCCAAAGGAAGCAAAATATAGAAACCAAGCTAGCTCAAAAAATCTGACTTTATCTGGA	1660
Qy	1561	ACCATCACTTTATTTGGAACCGGACGGGCGCTTTTATGAAATCATATAGTTTATAGAAATCTCT	1620
Db	1661	ACCATCACTTTATTTGGAACCGGACGGGCGCTTTTATGAAATCATATAGTTTATAGAAATCTCT	1720
Qy	1621	CAGTCTTACGACATCTTATAGAGCTCAAAAGCTTCTGGAACCTGTAAACAGCAACGCACTGAT	1680
Db	1721	CAGTCTTACGACATCTTATAGAGCTCAAAAGCTTCTGGAACCTGTAAACAGCAACGCACTGAT	1780
Qy	1681	CCAGATCCCTAATATGGGTGAGAAATTCCTAATACGGCTATCAGGGAACTTGGGGCCCAATT	1740
Db	1781	CCAGATCCCTAATATGGGTGAGAAATTCCTAATACGGCTATCAGGGAACTTGGGGCCCAATT	1840
Qy	1741	GTTTGGGGGACAGGGGCTTACAGCATCGCAACCTTCAACTGGAATTAACCTGGCTATATTT	1800
Db	1841	GTTTGGGGGACAGGGGCTTACAGCATCGCAACCTTCAACTGGAATTAACCTGGCTATATTT	1900
Qy	1801	CCTAATCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTTATGGAATGCATTTATAGAT	1860
Db	1901	CCTAATCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTTATGGAATGCATTTATAGAT	1960
Qy	1861	ATTAGCTCTCTCCATTTATCTTATGAGAGCTGCACACGAAAGGTTTGCAGGGAGACCGTGTCT	1920
Db	1961	ATTAGCTCTCTCCATTTATCTTATGAGAGCTGCACACGAAAGGTTTGCAGGGAGACCGTGTCT	2020
Qy	1921	TTTTGGTGTGCTCGATATCTAATCTTCTTCATAGAGATAGTACAAAAACGACGCGGG	1980
Db	2021	TTTTGGTGTGCTCGATATCTAATCTTCTTCATAGAGATAGTACAAAAACGACGCGGG	2080
Qy	1981	TTTCGCCAATTTGAGTGGCGGTTATGTCTATAGAGAGAAACCTACATATCTGTTCAGATAAG	2040
b	2081	TTTCGCCAATTTGAGTGGCGGTTATGTCTATAGAGAGAAACCTACATATCTGTTCAGATAAG	2140
y	2041	ATTCTTAGTGTGCTGATTTTGTGACGCTTTTGAAGAGATAGAGTACTACTTTGTAGCTAAG	2100
b	2141	ATTCTTAGTGTGCTGATTTTGTGACGCTTTTGAAGAGATAGAGTACTACTTTGTAGCTAAG	2200
y	2101	AATCAAGGTACGCTTACGAGGAACTCTCTATATACAGCAACACGAAAACCTATATCTCT	2160
b	2201	AATCAAGGTACGCTTACGAGGAACTCTCTATATACAGCAACACGAAAACCTATATCTCT	2260
y	2161	CTTCTTGTGCAAACTACGGCCCTTTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTC	2220
b	2261	CTTCTTGTGCAAACTACGGCCCTTTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTC	2320
y	2221	TTTTTCAGGAACCTTAGCTACACCCATACGGATACGATCTGAAAAACCAAGTATACAAACA	2280
b	2321	TTTTTCAGGAACCTTAGCTACACCCATACGGATACGATCTGAAAAACCAAGTATACAAACA	2380
y	2281	TATCTTACTGTAAAGGAAGCTCGGGGAATGATAGTTTCGCTTTAGTAATTCGGTGGGAAGA	2340
b	2381	TATCTTACTGTAAAGGAAGCTCGGGGAATGATAGTTTCGCTTTAGTAATTCGGTGGGAAGA	2440
y	2341	GTCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAAGTACATGCCCTTTCATGAAATTG	2400
b	2441	GTCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAAGTACATGCCCTTTCATGAAATTG	2500
y	2401	CAGTTTGTCTATGACATCAGGAAGGTTTTAAAGAACAGGGAAACAGAGCTCTGGAATTT	2460
b	2501	CAGTTTGTCTATGACATCAGGAAGGTTTTAAAGAACAGGGAAACAGAGCTCTGGAATTT	2560
y	2461	GGAAAGTAGCCGCTCTTGTGGAATCTTGGCTTACCTATCGGATCCGATTTTGATTAAGGAATCA	2520

Search completed: December 3, 2003, 09:21:23
Job time : 4 secs